Journal of Forestry Research (2010) 21(4): 487–491
DOI 10.1007/s11676-010-0103-2

ORIGINAL PAPER

Variability in growth characteristics for different genotypes of *Eucalyptus tereticornis* (SM.)

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Received: 2009-05-01; Accepted: 2010-06-01

Abstract: Eighteen clones of *Eucalyptus tereticornis* (Sm.) were evaluated for three years by adopting randomized block design for various growth parameters at Hoshiarpur, Punjab, India and compared with two checks. Significant variations were recorded for height, diameter at breast height (DBH) and clear bole height (CBH). The broad sense heritability was low to moderate for both height and CBH. The genetic gain for height and CBH increased substantially *per se* with the increase in age of trees. The average genetic gain for three years was recorded maximum for height (159.60%) followed by DBH (110.97%) and CBH (70.34%). Clone 17 attained maximum DBH over other genotypes for second and third year followed by clones 14 and 11. Clone 5 showed an upward trend for DBH and maintained its superiority for CBH as the age of the tree increased. Similarly, clone 11 changed its ranking from 9th to 8th to 3rd for DBH and from 9th to 4th to 2nd for CBH, respectively for the age of one, two and three years. Nonetheless, clones 6 and 10 performed poorly for all the characters studied. Clones 17, 14 and 5 were found to be the most promising clones for commercial deployment.

Keywords: *Eucalyptus tereticornis*; clones; heritability; genetic advance; genetic gain

Introduction

The genus *Eucalyptus* belongs to the family Myrtaceae and comprises about 700 species (Eldridge et al. 1993), and in India mainly two species *viz. E. tereticornis* and *E. camaldulensis* have been planted extensively owing to their faster growth rate and short rotation for various end uses including pulp, wood, sawn timber, fencing pole, firewood and extraction of aromatic oils (Lal 2000). Though millions of seedlings of eucalypt are being planted every year, the productivity has not been commensurating with the expected yield mainly due to poor quality of planting stock. In fact, the requirement of various woods in India by 2010 AD has been projected to 344 million tonnes of fuel wood and charcoal, 37 million m^3 of industrial wood, 33 million m^3 sawn timber, 5.7 million m^3 pulp and paper wood and 1.3 million tonnes of wood based panels (Anon 1991; Lal 2000). In fact, the Ministry of Environment and Forests, Government of India in its 'State of Environment Report' indicated that India occupies 2.41% of the world's land area, of which 39% is degraded (Karthawinata et al. 2000), but has to meet the demand of 16.40% of the world's populations. Unsustainable land use practices have unfortunately been contributing immensely to such high degradation of available geographical land mass (Anon 2009). The situation has been alarming and immediate steps are required to increase the productivity of forests substantially either by enhancing the total forest cover or per unit area. Ironically, it may not be feasible to increase forest cover with large population size, and the possible option to bridge the gap is to enhance the productivity of existing forests and plantations by adopting clonal forestry under various afforestation programmes.

Short rotation forest tree species like eucalyptus can play a complementary role in bridging the gap between demand and supply. The species exhibits enormous genetic variability and differs significantly in quantitative and qualitative traits. The assessment of genetic variability is a key to progress in tree improvement (Zobel, 1981) and is a useful tool in determining the strategies for tree improvement and breeding of an important species like eucalyptus. The plantations established from genetically uniform material are highly venerable to major climatic factors or epidemic particularly for insects and diseases (Aradhya and Phillips 1993). Using the variability, significant improvement in the productivity of eucalyptus has been achieved in many countries through the application of various genetic tools coupled with clonal forestry, as the transfer of both additive and

The online version is available at http://www.springerlink.com

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Responsible editor: Yu Lei

non-additive characters is routinely possible. The approach is particularly attractive in capturing gains for traits that have low heritability (Zobel 1981) and also in the exploitation of heterosis. Using the approach, substantially higher productivity of eucalyptus has been achieved in Congo and Brazil. Aracruz Florestal Company, Brazil could achieve dramatic yield increment upto 100 $m^3 \cdot ha^{-1} \cdot a^{-1}$ in clonal plantations. Even in India, the productivity of some of the *Eucalyptus* clones under un-irrigated conditions has been reported to about 20-25 $m^3 \cdot ha^{-1} \cdot a^{-1}$ (Lal 2000).

The present study purports to test the superiority of different clones for various growth parameters that ultimately influence the productivity of the species. Once the promising clones are identified in this species, the farmers, planters and paper-based industries could deploy these clones on commercial scale for industrial and domestic purposes.

Material and methods

A field trial consisting of 18 clones and two checks (one from the clonal seed orchard and one from unknown seed source) of *Eucalyptus tereticornis* was established at Hoshiarpur, Punjab (31º31'36"N latitude, 75º48'54"E longitude, 267.30 m altitude and 1242.2 mm rainfall) in Northern India. The plantations of the species are mostly raised either by collecting from seed from an unknown source or from the seed orchards. Therefore, it is inevitable to develop the clone(s) which perform better than the existing planting stocks, so that the productivity of newer plantations established with improved genetic material is enhanced to popularize among the growers. It was with this background that two checks used to understand comparative growth and productivity pattern of different clones. The evaluation trial was established by adopting completely randomised block design with three replication and twenty plants of each genotype in a block of 20 plants (5×4). The trial was established basically with a uniform spacing of 2 m × 2 m.

The clonal plants were raised by planting single nodal coppice cuttings treated with 2000 $\mu L \cdot L^{-1}$ Indole Butyric Acid (IBA) in 48 h pre-soaked vermiculite filled-in 150 mL root trainers. The root trainers were kept in the mist chamber for 45 days where 80%–85% relative humidity was maintained all the times. After 45 days, the rooted cuttings were weaned out first to the shade house with 75% shading and then to the open conditions gradually to harden the rooted cuttings. After 15 days of hardening, the plants were ready for field planting. At the same time, the seeds of the checks were also sown in 150-mL root trainers filled with above mentioned rooting media to ensure that the age of planting material for both clonal stock and seedling is uniform at the time of field planting. The trial was established in the field during 2005 and measured annually for height, diameter of breast height (DBH) and clear bole height (CBH) continuously for three years. The observations were collected upto the age three growing years, which were analyzed for different genetic parameters, using SAS (version 9.1.2 software for windows).

Analysis of variance: The observations were computed for analysis of variance (ANOVA) as per Sukhatme and Amble (1989).

Source of variation	Degree of freedom	Mean square	Expectation of mean square
Clones	C – 1	MS_C	$\sigma^2e + R\sigma^2c$
Replications	R – 1	MS_R	$\sigma^2e + C\sigma^2r$
Residual	(C - 1) (R – 1)	MS_E	σ^2e
Total	RC – 1	-	-

where, C and R are the number of clones and replications, respectively. Similarly σ^2e, σ^2c and σ^2r represent variance due to composite residual, clones and replications, respectively.

Variance: The genotypic and phenotypic components of variance were calculated from the ANOVA as described by Burton (1952).

Genotypic variance:

$$(\sigma^2 g)=((\sigma^2 e+R\sigma^2 c)-\sigma^2 e)/r$$

where r represents number of replications

Phenotypic variance:

$$(\sigma^2 p)=\sigma^2 g+\sigma^2 e$$

Genotypic Coefficient of variance:

$GCV = (\sqrt{\sigma^2 g} / mean) \times 100$

Phenotypic coefficient of variance:

$PCV = (\sqrt{\sigma^2 p} / mean) \times 100$

Heritability: Broad sense heritability was calculated as per Lush (1949).

$$h^2 = \sigma^2 g / \sigma^2 p$$

Genetic Advance: The genetic advance was calculated as described by Johnson et al. (1955).

$Gs = K. h^2. \sqrt{\sigma^2_p}$

where K is the selection intensity and calculated to 2.06

Genetic gain: The expected genetic gain, in per cent of mean, was calculated following Burton and Devane (1953).

Genetic gain = (Gs/mean) × 100

Results and discussion

The genetic parameters are very useful tools in predicting the amount of gain expected from clonal planting stocks and improved seed of clonal seed orchards. The variation among the clones is commonly used as an estimate of total genetic variation and used to calculate the degree of genetic control for a particular trait (Foster and Shaw 1988). Though the selection of superior trees / ortets was carried out using index method of selection with intensive selection criteria, genetic superiority *per se* needs to be determined to identify a genetically superior clones / genotypes. The yearly data obtained was analyzed and found that the average height of the clones ranged from 268 to 526 cm for first year, 482 to 814 cm for second year and 572 to 1031 cm for third

year, with a variation of 96.27%, 68.88% and 80.24% for first, second and third year, respectively. The DBH ranged from 1.82 to 4.39 cm for first year, 3.76 to 6.69 cm for second year and 4.64 to 8.00 cm for third year, with a variation of 141.21%, 79.36% and 72.41% for first, second and third year, respectively. Similarly, the clear bole height (CBH) ranged from 45 to 116 cm, 158 to 335 cm and 205 to 442 cm with 157.78%, 112.03% and 115.61% variability respectively for first, second and third years (Table 1).

Table 1. Mean values for different characters in *Eucalyptus tereticornis* (Sm.)

Genotype	First year			Second year			Third year		
	Height (m)	DBH (cm)	CBH(cm)	Height (m)	DBH (cm)	CBH (m)	Height (m)	DBH (cm)	CBH (m)
1	4.07±1.04	3.16±1.50	0.95±0.42	7.15±1.93	6.04±2.00	2.64±1.00	8.83±2.23	6.97±2.24	3.27±1.17
2	3.88±1.25	3.16±1.46	1.16±0.48	6.96±2.58	5.99±3.03	2.29±1.03	7.86±2.74	6.63±3.34	2.62±0.93
3	3.89±1.38	3.53±4.29	0.80±0.33	7.36±2.38	5.90±2.54	2.28±0.75	9.01±2.95	6.84±2.90	3.02±1.17
4	3.27±1.41	3.13±6.52	0.73±0.35	5.52±2.55	4.51±2.96	1.94±0.73	6.94±3.45	5.37±3.35	2.53±1.06
5	4.09±1.80	2.47±1.44	1.16±0.52	8.14±3.10	5.56±2.52	3.35±1.22	9.42±4.33	7.18±2.84	4.42±1.71
6	2.68±1.11	1.91±1.54	0.45±0.29	4.82±2.06	3.76±2.47	1.58±0.74	5.72±2.53	4.64±2.81	2.05±1.04
7	3.66±2.02	2.47±1.79	0.92±0.41	6.72±2.76	5.07±2.95	2.65±1.04	8.42±3.62	6.03±3.00	3.09±0.89
8	3.66±0.90	2.66±1.04	0.90±0.37	6.60±1.71	5.65±2.05	2.15±0.76	8.23±2.01	6.93±2.49	2.71±0.93
9	4.09±0.83	3.21±0.98	0.79±0.40	7.17±1.39	6.28±1.43	2.49±0.87	8.48±2.09	7.04±1.97	2.92±1.12
10	2.92±1.02	1.82±0.91	0.62±0.36	4.94±1.85	4.10±1.93	1.89±0.77	6.53±2.08	5.11±2.02	2.36±0.98
11	3.95±0.99	2.87±1.17	0.94±0.50	7.14±1.78	5.82±1.84	2.63±0.70	8.28±1.94	7.25±8.74	3.28±1.19
12	5.26±1.18	4.39±5.37	0.94±0.44	7.18±2.16	5.98±1.19	2.55±0.25	9.88±1.66	7.23±1.71	2.96±0.72
13	3.05±1.00	2.11±1.14	0.75±0.49	5.47±1.93	4.37±2.24	1.97±0.81	6.42±2.47	5.10±2.72	2.58±1.22
14	5.18±0.83	4.26±4.61	0.97±0.36	8.03±1.18	6.22±1.36	2.57±0.55	10.31±1.59	7.66±1.78	3.17±0.67
15	3.85±1.21	2.76±1.15	0.69±0.36	6.31±1.71	4.93±1.83	2.29±0.79	7.64±1.76	6.08±2.16	2.88±0.90
16	3.49±1.17	2.56±1.38	1.08±0.36	5.88±2.01	5.22±2.56	2.18±0.81	7.58±2.57	6.32±3.11	2.77±1.09
17	4.54±1.29	3.65±1.39	1.10±0.74	7.35±1.56	6.69±1.77	2.41±0.91	8.47±1.40	8.00±1.96	3.04±0.78
18	3.41±1.29	2.28±1.22	0.71±0.37	5.94±2.19	5.01±2.40	2.01±0.93	7.30±2.48	6.12±2.80	2.61±0.99
CSO Seedlot	4.11±1.60	2.74±1.19	0.97±0.41	7.17±2.46	5.46±2.53	2.59±0.72	9.19±3.52	6.75±3.00	3.27±1.11
Unknown Seedlot	3.67±1.35	2.58±1.72	0.82±0.41	6.95±1.91	5.30±1.95	2.51±0.75	8.51±2.19	6.28±2.23	3.19±0.89
Average	3.84	2.89	0.87	6.64	5.39	2.35	8.15	6.48	2.94
Maximum	5.26	4.39	1.16	8.14	6.69	3.35	10.31	8.00	4.42
Minimum	2.68	1.82	0.45	4.82	3.76	1.58	5.72	4.64	2.05
Std. Dev.	0.65	0.69	0.18	0.94	0.78	0.38	1.18	0.90	0.48

DBH, diameter at breast height; CBH, clear bole height

The analysis of variance (ANOVA) for different genotypes showed that the values are highly significant for all the parameters studies (Table 2). Accordingly, the variance (genetic and phenotypic), broad sense heritability, genetic advance and genetic gain for height, diameter at breast height and clear bole height were calculated and presented in Table 3. The genotypic and phenotypic coefficient of variation for all the characters provided evidences for existence of adequate genotypic variations. The analyzed results showed that height was the most important trait with maximum genotypic coefficient of variation for all three years of study followed by DBH and CBH (Table 3). The results thus indicate that both height and DBH are the principal characters for field evaluation of Eucalyptus and there is considerable inter genotypic variation exists for further genetic improvement.

The heritability expresses the degree to which a character is influenced by heredity as compared to the environment. Estimation of broad sense heritability for various characters (Table 3) showed low to moderate heritability for height (0.27, 0.28 and 0.48), DBH (0.13, 0.22 and 0.22) and CBH (0.18, 0.42 and 0.45) for all three years respectively. The results are in agreement with the studies carried out by Apiolaza et al. (2005) on *E. globules* to report low heritability (0.20) for DBH during field evaluation of eight sub-races in Tasmania. Similarly, low to moderate heritability was recorded in *E. globules* and *E. nitens* for different genetic parameters (Raymond 2002). The broad sense heritability for height and tree volume in *E. grandis* was not only low to moderate but also varied with changing environment and age (Osorio et al. 2001). Nelson and Tauer (1987) in poplars also reported moderate to high broad sense heritability for juvenile traits like height, diameter, growth and leaf size. Kumar (2007) also reported low to moderate heritability for height (0.31), diameter at ground level (0.44) and diameter at breast height (0.37), during field evaluation of 70 clones of *Gmelina arborea*. Nonetheless, there is a need to estimate narrow-sense heritability for individual growth components so that additive genetic variance associated with individual growth components is calculated. Thus these estimates usually facilitate selection on those traits from which a positive genetic response can be expected at reasonable selection intensity. In present study, the highest genetic

advance was observed for height (4.44, 9.27 and 18.25) followed by DBH (3.28, 5.60 and 7.47) and CBH (0.28, 1.82 and 2.98). In fact, the maximum average genetic gain (159.60 %) also reported for height followed by DBH (110.97 %) and CBH (70.34 %). Nonetheless, the genetic gain for third year was found to be maximum (223.62, 115.35 and 100.99) for the height, DBH and CBH, respectively, and was positive for all the traits. The genetic gain *per se* increased substantially as the age of the trees increased for height and CBH (Table 3).

Table 2. Analysis of variance for different traits of 20 genotypes of *Eucalyptus tereticornis*

Source of variation	Degrees of freedom	Mean sum of squares								
		Height			Diameter at breast height			Clear bole height		
		First year	Second year	Third year	First year	Second year	Third year	First year	Second year	Third year
Genotypes	19	25.54**	52.91**	83.24**	28.85**	36.33**	47.89**	2.06**	8.77**	13.94**
Replications	2	37.75	103.85	107.43	34.89	75.89	39.35	1.59	8.74	7.81
Residue	38	8.84	18.05	14.64	16.51	15.25	19.79	0.99	1.91	2.74

(** indicates level of significance at 1 percent)

Table 3. Different genetic parameters calculated for 20 genotypes of *Eucalyptus tereticornis* for three years of growth

Genetic parameters	Characters and yearly static								
	Height			Diameter at breast height			Clear bole height		
	First year	Second year	Third year	First year	Second year	Third year	First year	Second year	Third year
Genetic variance	3.34	6.97	13.72	2.47	4.21	5.62	0.21	1.37	2.24
Phenotypic variance	12.17	25.02	28.35	18.98	19.46	25.41	1.20	3.28	4.97
Heritability (broad sense)	0.27	0.28	0.48	0.13	0.22	0.22	0.18	0.42	0.45
Genetic advance	4.44	9.27	18.25	3.28	5.60	7.47	0.28	1.82	2.98
Genetic gain	115.75	139.44	223.62	113.58	103.98	115.35	32.71	77.32	100.99
Genotypic coefficient of variance	43.52	52.42	84.07	42.70	39.09	43.36	12.30	29.07	37.97
Phenotypic coefficient of variance	158.49	188.14	173.71	328.34	180.56	196.06	69.20	69.53	84.24

The heritability, genetic advance and genetic gain were estimated from an early age (12 months) to the age of log phase (36 months) after planting. The growth rate generally enters the log phase from third or fourth years of age, thus heritability estimates carried out after this age would be more reliable. Up to the age of 36 months, the increasing trend of heritability for all the traits is a positive sign and can be understood as pointer compared with the results expected at a later stage of the evaluation. The comparison of present results with upcoming results will also enable establishment of genetic and age-age correlations. Obviously, the results of present study would perceptively determine whether genetic analysis at early stage is reliable for making future perditions. If reliable, genetic assessment for other population could also be carried out with suitable correlations or the extent of relationship can be determined and suitable age-age correlations. The results of preset study show that the clone 12 attained maximum height (526 cm) and DBH (4.39 cm), whereas clone 5 attained maximum CBH (116 cm). In the second year, clone 5 attained maximum height (814 cm) and CBH (335), whereas clone 17 attained maximum DBH (6.69 cm). Similarly, in third year clone 14 was found to attain maximum height (1031 cm), clone 17 attained maximum DBH (8.00 cm) and clone 5 with maximum CBH (442 cm). Clone 6 and 10 found to be the least performers consistently for all the traits during entire study period. Clone 5 was therefore the best performers for all the characters and showed consistency in growth, and improved its performance along the age. Similar trend was recorded for clones 17 and 14. These clones performed much better than that of the checks and could therefore play a significant role if planted on large scale commercially. However, their superiority needs to be tested over some more period of time to make suitable recommendations.

The clones in terms of mean DBH for all the years of assessment were compared for their change in ranking within themselves (Table 4). Clone 17 was ranked 3rd in the first year but out performed all the clones during 2nd and 3rd year of assessment to rank 1st. Clones 11, 5, and 18 recorded an upward trend whereas clones 3, 4 and 6 demonstrated a decreasing trend. Though the average increment for these clones over mean DBH from 1st to 3rd year was 125%, the clones 11, 8, 16, 5, 18, 10 and seed from CSO reported an increment of 153%, 161%, 147%, 191%, 168%, 181% and 146% respectively. The clones 3, 4 and 6 (decreasing trend) showed increment of 94%, 72% and 143% respectively.

While developing similar relationship for CBH, clone 5 maintained its superiority over all the genotypes. Clones 11, seed from CSO and unknown source changed ranking from 9th, 6th and 12th to 2nd, 4th and 5th positions. However, there was a sharp decrease in the ranking of clone 2 from 2nd position in first year to 15th in third year. The decreasing trend was also recorded for clones 13 and 4 (Table 5). Clones 10 and 6 performed poorly and maintained lowest positions for entire duration of field evaluation.

Table 4. Change in rank for different genotypes of *Eucalyptus tereticornis* on the basis of DBH

Rank	First year		Second year		Third year	
1	4.39	(12)	6.69	(17)	8.00	(17)
2	4.26	(14)	6.28	(09)	7.66	(14)
3	3.65	(17)	6.22	(14)	7.25	(11)
4	3.53	(03)	6.04	(01)	7.23	(12)
5	3.21	(09)	5.99	(02)	7.18	(05)
6	3.16	(01)	5.98	(12)	7.04	(09)
7	3.16	(02)	5.90	(03)	6.97	(01)
8	3.13	(04)	5.82	(11)	6.93	(08)
9	2.87	(11)	5.65	(08)	6.84	(03)
10	2.76	(15)	5.56	(05)	6.75	(COS)
11	2.74	(COS)	5.46	(COS)	6.63	(02)
12	2.66	(08)	5.30	(SL)	6.32	(16)
13	2.58	(SL)	5.22	(16)	6.28	(SL)
14	2.56	(16)	5.07	(07)	6.12	(18)
15	2.47	(05)	5.01	(18)	6.08	(15)
16	2.47	(07)	4.93	(15)	6.03	(07)
17	2.28	(18)	4.51	(04)	5.37	(04)
18	2.11	(13)	4.37	(13)	5.11	(10)
19	1.91	(06)	4.10	(10)	5.10	(13)
20	1.82	(10)	3.76	(06)	4.64	(06)
Mean	2.89		5.39		6.48	

Figures in parenthesis are the genotypes

Table 5. Change in rank for different genotypes of *Eucalyptus tereticornis* on the basis of CBH

Rank	First year		Second year		Third year	
1	1.16	(05)	3.35	(05)	4.42	(05)
2	1.16	(02)	2.65	(07)	3.28	(11)
3	1.10	(17)	2.64	(01)	3.27	(01)
4	1.08	(16)	2.63	(11)	3.27	(CSO)
5	0.97	(14)	2.59	(CSO)	3.19	(SL)
6	0.97	(COS)	2.57	(14)	3.17	(14)
7	0.95	(01)	2.55	(12)	3.09	(07)
8	0.94	(12)	2.51	(SL)	3.04	(17)
9	0.94	(11)	2.49	(09)	3.02	(03)
10	0.92	(07)	2.41	(17)	2.96	(12)
11	0.90	(08)	2.29	(02)	2.92	(09)
12	0.82	(SL)	2.29	(15)	2.88	(15)
13	0.80	(03)	2.28	(03)	2.77	(16)
14	0.79	(09)	2.18	(16)	2.71	(08)
15	0.75	(13)	2.15	(08)	2.62	(02)
16	0.73	(04)	2.01	(18)	2.61	(18)
17	0.71	(18)	1.97	(13)	2.58	(13)
18	0.69	(15)	1.94	(04)	2.53	(04)
19	0.62	(10)	1.89	(10)	2.36	(10)
20	0.45	(06)	1.58	(06)	2.05	(06)

Figures in parenthesis are the genotype

The trend in ranking of different genotypes indicates that the field evaluation and testing of these clones needs to be carried out for longer duration, so that elite genotypes are screened and deployed through plantations programmes. It is also necessary to examine the trend of all the clones over the years as to group different clones on the basis of end uses. The early starters could well be used to raise biomass plantations for paper industry, whereas slow starters may be recommended for timber and furniture industry. However, individual clones need to be analysed for different wood properties before recommending their deployment through plantations programmes. Nonetheless, described results indicate clonal growth pattern of different clones at a single location and needs to be tested for real the analysis of adaptability through G×E interaction and superiority *per se*.

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